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May 7, 2002, 12:08:26 ; Search time 54.19 Seconds (without alignments) 383.293 Million cell updates/sec
                                                                                                                                                                                                           1 MAVLVLFLCLVAFPSCVLSQ......MKRGYAMDYWGQGTLVTVSS 142
                                                                                                                                                                                                                                                                                                                                                  473505
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    473505 seqs, 146272329 residues
                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                           US-09-772-103-10
                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPTREMBL_17:*
: sp_archea:*
: sp_bacteria:*
                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                        Perfect score:
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                                                                                                                                                                                                           Sequence:
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                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_plant:*
sp_rodent:*

sp_phage:*

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*

homo sapien homo sapien 2 mus musculu 099ng4 mus musculu homo sapien homo sapien homo sapien homo sapien 099ka4 mus musculu 09u172 homo sapien 09n0w6 oryctolagus 09ul73 homo sapien 095973 homo sapien sapien sapien sapien sapien sapien sapien 299m22 muss 29u136 homo s 29u136 homo s 29hcc1 homo s 29u193 homo s 29u193 homo s 29u184 homo s 29u171 homo s 29u171 homo s 29u174 homo s 29u184 homo s Q9bul0 homo Q9bqb8 homo Description SUMMARIES Q9UL73 095973 Q9BU10 Q9BQBB Q99M22 Q99NG4 Q99KA4 Q9UL72 Q9N0W6 Q9UL96 Q9UL75 09HCC1 09UL93 09UL90 09UL88 09UL88 Q9UL92 Q9Y509 Q9UL84 ΙD Query Match Length DB Score 437 429 427 392.5 374 346.5 323 321 319.5 318.5 317.5 317.5 317.5 No. Result

140 VSS 142

QΥ

Q9d814 mus musculu Q9n0w4 oryctolagus Q9r1a4 mus musculu Q9r131 homo sapien Q99131 homo sapien Q99131 mus musculu Q9gyf6 mus musculu Q9gyf6 mus musculu Q991a4 homo sapien Q991A7 mus musculu Q911A7 homo sapien Q911A7 homo sapien Q941A7 homo sapien Q941A7 homo sapien Q941A7 homo sapien Q941A8 mus musculu Q941A7 homo sapien Q941A9 homo sapien Q941B9 homo sapien Q941B9 homo sapien Q941B9 homo sapien Q941B9 homo sapien Q941B8 mus musculu Q951A7 mus musculu Q951A8 mus musculu Q951B8 mus musculu Q951B8 mus musculu Q951B8 mus musculu Q951B8 mus musculu	ALIGNMENTS PRT; 121 AA. reated) ist sequence update) ist annotation update) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. 99; e M., Baensch M., Sohns B., Arseniev L., tibodies from Phage Display Libraries.";). D293E4EBC8C59D5B CRC64;	tch 62.3%; Score 462.5; DB 11; Length 121; 90; Conservative 10; Mismatches 20; Indels 3; Gaps 1; OVOLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWYRQPPGKGLEWLGVIWAGGTUYN 79
Q9D8L4 Q9N0W4 Q9N1A4 Q9UL91 Q99L31 Q9QXFQ Q99LC4 Q99LA6 Q99LD5 Q99LD5 Q99LD7 Q90LD7 Q90LD7 Q90LD5		Score 462.5; Pred. No. 7.5); Mismatches); Mismatches SGFSLTSYGVWW SGFPLTSHGVSWW. VTAADTAVYYCAR :
11	17, c 17, 1 17, 1 17, 1 17, 1 11, 1 11, 1 11, 1 11, 1	%; %; 10 ICTV; IICTV; KLSSY KLSSY
473 473 474 473 468 298 298 484 484 473 1119 1119 1119 1110 1110 1110 1110 111	LIMINARY; EWBLrel. 17, Ci EMBLrel. 17, Li EMBRANT). Use). Luse). A. A	62.38 Conservative Conservative SGPGLVRESQTLSIT
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310 309.5 308.5 308.5 306.5 306.5 303.3 303.5 295.5 295.5 291.5 29	1 1 1 1 1 1 1 299NG4 PRELI 299NG4 299NG4 299NG4 209NG4 209NG4 200NG-2001 (TrEM OI-JUN-2001	מ ט
22222222222222222222222222222222222222	ULT Q9 Q9 Q9 Q1 Q1 Q1 Q1 Q1 Q1 Q1 Q1 Q1 Q1	Query M Best Lo Matches 20 20 80 61
	RESULT Q99NG4 ID Q99NG4 ID Q99NG4 DT Q11 DDT Q1	Ou Be Ma Qy Db

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EMBL; AF103795; AAC79084.1; -. HSSP; P01825; 7FAB.
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                                                                                                       Signal.
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Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
"Clonal proliferation of 1gM secreting B cell in the synovium of Behcet's patient with arthritis.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 SALMSRLTISKDISKNQVSLKLSSVTAADTAVYYCAR----GPPHAMMKRGYAMDYWGQG 135
                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 69.3%; Pred. No. 2.6e-36;
Matches 88; Conservative 11; Mismatches 16; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLQESGPCLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWLGVIWAGGTTNYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSETLSLTCTVSGGSICSYYWSWIRQPPGKGLEWIGYIYYSGSINYT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER 119 119 SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
VH4 HEAVY CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
                                                                                             119 AA
                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
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                                                                                                                                                                                                                                                                                          MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF035041; AAD56277.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 TLVTVSS 119
                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                 118 VSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.8%; Score 429; DB 4; Length 597;
62.4%; Pred. No. 1e-34;
tive 12; Mismatches 32; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 PPGKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGP 118
                                                                                                                                                                                                                                                                                                                             9; Gaps
                                                                                                                                                                                                                                                                                                        1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVY--WVRQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                     58.7%; Score 435.5; DB 4; Length 150; 64.6%; Pred. No. 4.8e-36; Live 15; Mismatches 27; Indels 9
                                                                                                                     VH4 HEAVY CHAIN VARIABLE REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC002963; AAH02963.1; -. SDAFA8FB7E055851 CRC64; SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                              150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AMMKRG-----YAMDYWGOGTLVTVSS 142
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01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 PHAMMKRGYAMDYWGQGTLVTVSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 ---- LGMG-AFDFWGHGTMVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNKNOWN (PROTEIN FOR MGC:1652).
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                      Best Local Similarity 64.6%
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                        19
>150
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Best Local Similarity
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61 GKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPP 60
                                                                                                                                                                                                                                                                                                                                                                                                                      59 PPGKGLEWLGVIWAGGTTNYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAVLVLFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVY--WVRQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.9%; Score 392.5; DB 11; Length 479; 58.6%; Pred. No. 3.5e-31; tive 18; Mismatches 29; Indels 13;
                                                                                                                                                                                                                                                                                                                                          ; Score 427; DB 4; Length 597;
; Pred. No. 1.6e-34;
11; Mismatches 33; Indels :
                                                                                                                                                                    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                           Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006180; AAH06180.1; -.
EMBL; BC001872; AAH01872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                  1872; AAH01872.1; -.
597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN (PROTEIN FOR MGC:6342).
                                                                                                                                                                                                                                                                                                                                            57.5%;
62.4%;
                                                                                                                                                                                                                                                                                                                                                                       93; Conservative
                                                                                                                     SEQUENCE FROM N.A.
TISSUE-RHABDOMYOSARCOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=MAMMARY TUMOR;
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                                TISSUE=LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                        NCBI_TaxID=9606;
                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                 Strausberg R.;
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                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                       Query Match
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Q99M22
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                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 YNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPHAMMKRGYAMDYWGQGTL 137
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.4%; Score 374; DB 4; Length 121; Best Local Similarity 60.8%; Pred. No. 5.2e-30; Matches 76; Conservative 14; Mismatches 29; Indels
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Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                           121 AA.
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PRT;
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EMBL; AF035018; AAD56254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                         PRELIMINARY;
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-----RRYALDYWGQGTLV 112
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MEDLINE=98277139; PubMed=9614934;
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MEDLINE=98277139; PubMed=9614934;
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Best Local Similarity
Matches 64; Conservat
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Q9UL93
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"An antibody fragment2A3 specific for native lysozyme :Isolaion from a human synthetic phage display library and characterization.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                   -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 ÅSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPHAMMKRGYAMDYWGQGTLV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWL-GVIWAGGTTNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                               Score 346.5; DB 4; Length 122;
Pred. No. 3e-27;
7; Mismatches 27; Indels 9
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122 AA; 13719 MW; 56CB0612586A6529 CRC64;
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SINGLE CHAIN FV FRAGMENT (FRAGMENT).
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46.7%; Score 346.5; I
Best Local Similarity 58.3%; Pred. No. 3e-27
Matches 74; Conservative 17; Mismatches
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                                                                            EMBL; AF035039; AAD56275.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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InterPro; IPR003600; 19_11ke.
InterPro; IPR00306; 19_MHC.
InterPro; IPR003596; 19_V.
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SMART: SM00409; IG; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
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Clin. Immunol. Immunopathol. 87:184-192(1998).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 SALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPHAMMKRGYAMDYWGQGTLVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 VQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWLGVI-WAGGTTNYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.9%; Score 326; DB 4; Length 11052.0%; Pred. No. 3.1e-25;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                            79 NSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPHAMMKRGYAMDYWGQGTLV 138
                                                                                                                                                  Match 43.5%; Score 323; DB 4; Length 113; Local Similarity 50.8%; Pred. No. 6.1e-25; Conservative 22; Mismatches 27; Indels 12; Gaps
                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                       20 QVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWLGVI-WAGGTTNY 78
                                                                                                                                                                                                                       :| : : |||||:||:||| : |:::|: |||||||| | :: : : :|
61 DYAAPVKGRLTISRDSSKNTLYLRMNSLKTEDTAVYYCTTGITMIIVVITTSSKRTSFEY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 NYNSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPHAMM-----KRGYAMDY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWLGVIWA---GGTT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.5%; Score 323; DB 4; Length 131; 50.4%; Pred. No. 7.2e-25; ative 23; Mismatches 34; Indels
                                                                              NON_TER 1 13 1 13 NON_TER 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 131 131
SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
        EMBL., AF035024; AAD56260.1; -
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF035026; AAD56262.1; ... InterPro; IRR003006; Ig_MHC. InterPro; IPR003596; Ig_V. Pfam, PF0047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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01-MA-2000 (TrEMBLrel. 13, Created)
01-MA-2000 (TrEMBLrel. 13, Last sequence update)
01-MV-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 NSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARGPPHAMMKRGYAMDYWGQGTLV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: | |||:| ||| : |:::|: | ||||:|
61 ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIYDR---FDIWGQGTMV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWLGVIWA-GGTTNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                              Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.3%; Score 321; DB 4; Length 121; 50.8%; Pred. No. 1e-24; tive 22; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                           121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; . 124 AA.
                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                             EMBL; AF035043; AAD56279.1; --
HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 50.89
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SMART; SM00406; IGv; 1.
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121 WGQGTLVTVSS 131
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                 DOMAIN.
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                                                                                                                                                                                                                                                                                             fetus."
                                                                             Q9UL71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 QVQLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWLGVI-WAGGTTNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGLYVVVPAAFSR----FDYWGQ 116
                                                                                                                                                                                                                                                                                                                                                                                     79 NSALMSRLTISKDTSKNQVSLKLSSVTAADTAVYYCARG----PPHAMMKRGYAMDYWGQ 134
                                                                                                                                                                                                                                                                                                                                     20 QVOLQESGPGLVKPSQTLSLTCTVSGFSLTSYGVYWVRQPPGKGLEWLGVI-WAGGTTNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                       Query Match 43.1%; Score 319.5; DB 4; Length 124: Best Local Similarity 49.2%; Pred. No. 1.5e-24; Matches 63; Conservative 27; Mismatches 29; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;
                                                                                                                                                                         NON_TER 124 124
SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
VH3 PROTEIN (FRAGMENT).
                                                              EMBL, AF035022, AAD56258.1; -. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; Ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S80860; AAD14339.1; -. HSSP; P01772; 2FB4.
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InterPro; IPR003596; Ig_V.
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Best Local Similarity
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Q9Y509
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Db 61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAKDGNY-FDSVGYYAGIDYWGQG 119
QY 136 TLVTVSS 142
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Db 120 TLVTVSS 126
Search completed: May 7, 2002, 12:08:26
JOb time: 454 sec
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